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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/058,053A

DATE: 07/23/2002

TIME: 15:59:19

Input Set : A:\2314-248-rev.ST25.txt

Output Set: N:\CRF3\07232002\J058053A.raw

6-8

3 <110> APPLICANT: University of Utah Research Foundation
4 Cognetix, Inc.
5 Jones, Robert M.
6 Garrett, James E.
7 Watkins, Maren
8 Olivera, Baldomero M.
10 <120> TITLE OF INVENTION: B-Superfamily Conotoxins
12 <130> FILE REFERENCE: 2314-248
14 <140> CURRENT APPLICATION NUMBER: US 10/058,053A
C--> 15 <141> CURRENT FILING DATE: 2002-07-05
17 <150> PRIOR APPLICATION NUMBER: US 60/264323
18 <151> PRIOR FILING DATE: 2001-01-29
20 <160> NUMBER OF SEQ ID NOS: 340
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 456
26 <212> TYPE: DNA
27 <213> ORGANISM: Conus flavidus
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35 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp
36 1 5 10
38 att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96
39 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg
40 15 20 25 30
42 ggt ttg gtg cca gat gac tta acc cca cag ctt att ttg caa agt ctg 144
43 Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu
44 35 40 45
46 gat tcc cgt cgt cat gat cac ggc att cgt ccg aag aga gtc gac ata 192
47 Asp Ser Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile
48 50 55 60
50 tgt aac tgg agg ata tgt gca cca aac cca ttg aga cga cat gat ctt 240
51 Cys Asn Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu
52 65 70 75
54 aag aaa gga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcgtt 295
55 Lys Lys Gly Asn Asn
56 80
58 aatcagactt cagcaaatat gaaattttca gcatcactgt gggtgtgaag aaatcagttg 355
60 ctttaaaagg ttggatttgt ccttgtttaa gccgttgtac tgatgacatc tctgcactat 415
62 gaaataaagc tgatgtgaca aactaaaaaa aaaaaaaaaa a 456

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Input Set : A:\2314-248-rev.ST25.txt

Output Set: N:\CRF3\07232002\J058053A.raw

65 <210> SEQ ID NO: 2

66 <211> LENGTH: 83

67 <212> TYPE: PRT

68 <213> ORGANISM: Conus flavidus

70 <400> SEQUENCE: 2

72 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr

73 1 5 10 15

76 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu

77 20 25 30

80 Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu Asp Ser

81 35 40 45

84 Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile Cys Asn

85 50 55 60

88 Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu Lys Lys

89 65 70 75 80

92 Gly Asn Asn

96 <210> SEQ ID NO: 3

97 <211> LENGTH: 33

98 <212> TYPE: PRT

99 <213> ORGANISM: Conus flavidus

101 <220> FEATURE:

102 <221> NAME/KEY: PEPTIDE

103 <222> LOCATION: (1)..(33)

104 <223> OTHER INFORMATION: Xaa at residues 7, 20 and 22 may be Pro or hydroxy-Pro; Xaa at re

105 residue 15 may be Trp (Dor L) or bromo-Trp (Dor L)

108 <400> SEQUENCE: 3

W-1> 110 His Asp His Gly Ile Arg Xaa Lys Arg Val Asp Ile Cys Asn Xaa Arg

111 1 5 10 15

W-1> 113 Ile Cys Ala Xaa Asn Xaa Leu Arg Arg His Asp Leu Lys Lys Gly Asn

114 20 25 30

116 Asn

119 <210> SEQ ID NO: 4

120 <211> LENGTH: 374

121 <212> TYPE: DNA

122 <213> ORGANISM: Conus miles

124 <220> FEATURE:

125 <221> NAME/KEY: CDS

126 <222> LOCATION: (7)..(315)

128 <400> SEQUENCE: 4

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130 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val

131 1 5 10

133 ggg ctc acc gtc ggg agt cac gtc cat cgg tct cac agt cct aca tcg 96

134 Gly Leu Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser

135 15 20 25 30

137 cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat 144

138 Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His

139 35 40 45

141 ctg ttt gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg 192

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142 Leu Phe Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val
143          50          55          60
145 gat ctt cct gca ggg aat ggt gca ggc aac acc aag caa caa gac caa      240
146 Asp Leu Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln
147          65          70          75
149 agt cct cat cat gtg tgt tgt gct att ggt ccg gtt ctt cca ttc tgt      288
150 Ser Pro His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys
151          80          85          90
153 tgt gtc agt tgg ctg cac aaa ctc cat tgaactggcc aatgaaaata      335
154 Cys Val Ser Trp Leu His Lys Leu His
155 95          100
157 actcaggaat agacagaaag gcaaaaaaaaaa aaaaaaaaaa      374
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 103
162 <212> TYPE: PRT
163 <213> ORGANISM: Conus miles
165 <400> SEQUENCE: 5
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168 1          5          10          15
171 Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
172          20          25          30
175 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
176          35          40          45
179 Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
180          50          55          60
183 Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln Ser Pro
184 65          70          75          80
187 His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys Cys Val
188          85          90          95
191 Ser Trp Leu His Lys Leu His
192          100
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 29
197 <212> TYPE: PRT
198 <213> ORGANISM: Conus miles
200 <220> FEATURE:
201 <221> NAME/KEY: PEPTIDE
202 <222> LOCATION: (1)..(29)
203 <223> OTHER INFORMATION: Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 6, 15
and 18
204          may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp (D or L)
205          or bromo-Trp (D or L)
208 <400> SEQUENCE: 6
W--> 210 Xaa Gln Asp Gln Ser Xaa His His Val Cys Cys Ala Ile Gly Xaa Val
211 1          5          10          15
W--> 213 Leu Xaa Phe Cys Cys Val Ser Xaa Leu His Lys Leu His
214          20          25
216 <210> SEQ ID NO: 7
217 <211> LENGTH: 359
218 <212> TYPE: DNA

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Output Set: N:\CRF3\07232002\J058053A.raw

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219 <213> ORGANISM: Conus miles
221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (7)..(291)
225 <400> SEQUENCE: 7
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228      1          5          10
230 ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg      96
231 Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser
232 15          20          25          30
234 cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat      144
235 Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His
236          35          40          45
238 ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg      192
239 Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val
240          50          55          60
242 gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa      240
243 Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln
244          65          70          75
246 aga cgt ctc tgc tgc atc ttt gcc ccg att ctt tgg ttc tgt tgt cac      288
247 Arg Arg Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His
248      80          85          90
250 ggt taacagctca aattacactg cactggccga ttgaaagaac tgcaataaac      341
251 Gly
252 95
254 ggaaaaaaaaa aaaaaaaaaa      359
257 <210> SEQ ID NO: 8
258 <211> LENGTH: 95
259 <212> TYPE: PRT
260 <213> ORGANISM: Conus miles
262 <400> SEQUENCE: 8
264 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
265 1          5          10          15
268 Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
269          20          25          30
272 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
273          35          40          45
276 Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
277          50          55          60
280 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg
281 65          70          75          80
284 Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His Gly
285          85          90          95
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 14
290 <212> TYPE: PRT
291 <213> ORGANISM: Conus miles
293 <220> FEATURE:

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RAW SEQUENCE LISTING

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TIME: 15:59:19

Input Set : A:\2314-248-rev.ST25.txt

Output Set: N:\CRF3\07232002\J058053A.raw

294 <221> NAME/KEY: PEPTIDE
 295 <222> LOCATION: (1)..(14)
 296 <223> OTHER INFORMATION: Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residue
 10 may
 297 be Trp (D or L) or bromo-Trp (D or L)
 300 <400> SEQUENCE: 9
 302 Leu Cys Cys Ile Phe Ala Xaa Ile Leu Xaa Phe Cys Cys His
 303 1 5 10
 305 <210> SEQ ID NO: 10
 306 <211> LENGTH: 351
 307 <212> TYPE: DNA
 308 <213> ORGANISM: Conus capitaneus
 310 <220> FEATURE:
 311 <221> NAME/KEY: CDS
 312 <222> LOCATION: (7)..(291)
 314 <400> SEQUENCE: 10
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 316 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val
 317 1 5 10
 319 ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg 96
 320 Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser
 321 15 20 25 30
 323 cgc agc cat ggt gat gac tcc att cat gac gag acg att cat caa cat 144
 324 Arg Ser His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His
 325 35 40 45
 327 ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg 192
 328 Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val
 329 50 55 60
 331 gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa 240
 332 Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln
 333 65 70 75
 335 aga ggt ttc tgc tgc gac ttt ccc ccg att ttt tgg ttc tgt tgt atc 288
 336 Arg Gly Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile
 337 80 85 90
 339 ggt taacagcaca aattacactg cactggccga ttgaaagaac tgcaataaac 341
 340 Gly
 341 95
 343 ggaaaaaaaaa 351
 346 <210> SEQ ID NO: 11
 347 <211> LENGTH: 95
 348 <212> TYPE: PRT
 349 <213> ORGANISM: Conus capitaneus
 351 <400> SEQUENCE: 11
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 354 1 5 10 15
 357 Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
 358 20 25 30
 361 His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His Leu Phe
 362 35 40 45
 365 Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/058,053A

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 TIME: 15:59:20

Input Set : A:\2314-248-rev.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 7,15,20,22
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 Seq#:9; Xaa Pos. 7,10
 Seq#:12; Xaa Pos. 7,8,11
 Seq#:15; Xaa Pos. 7,11,16,17
 Seq#:16; N Pos. 347,385,386
 Seq#:18; Xaa Pos. 7,15,20,26,27,29
 Seq#:21; Xaa Pos. 16,20,21,23
 Seq#:24; Xaa Pos. 16,20,21,23,24,27
 Seq#:27; Xaa Pos. 10,16,20,21,23,24
 Seq#:28; N Pos. 425,426
 Seq#:30; Xaa Pos. 7,10,14,18,19,21
 Seq#:33; Xaa Pos. 1,7,14,16,17,24,28,29,31,32,33,34
 Seq#:36; Xaa Pos. 1,7,9,14,20,21,29,30,33,43
 Seq#:39; Xaa Pos. 11,13,14,19
 Seq#:42; Xaa Pos. 1,14,16,17,24,28,29,31,32,33,34
 Seq#:45; Xaa Pos. 7,15,19,20,22,23
 Seq#:48; Xaa Pos. 16,20,23,24,27
 Seq#:51; Xaa Pos. 8,10,14,18,19
 Seq#:54; Xaa Pos. 7,15,19,20,22,23
 Seq#:57; Xaa Pos. 15,25,29,30,31,32,33
 Seq#:60; Xaa Pos. 16,20,21,22,23,24
 Seq#:63; Xaa Pos. 25,29,30,32,33
 Seq#:66; Xaa Pos. 16,20,21,23,24,27
 Seq#:69; Xaa Pos. 1,3,4,5,10,14,15,16,17,18
 Seq#:72; Xaa Pos. 1,6,10,14,15,17,18
 Seq#:75; Xaa Pos. 15,19,20,22
 Seq#:78; Xaa Pos. 13,17,18,19,20
 Seq#:81; Xaa Pos. 7,11,13,14,19,37,38
 Seq#:84; Xaa Pos. 3,14,18,19,20,21,22,25
 Seq#:87; Xaa Pos. 3,14,18,19,20,21,22,25
 Seq#:90; Xaa Pos. 14,21,24,29,30,31,33,43,45
 Seq#:93; Xaa Pos. 12,17,18,20,27,30
 Seq#:96; Xaa Pos. 12,17,18,20,25,27,30
 Seq#:99; Xaa Pos. 12,17,20,27,30
 Seq#:102; Xaa Pos. 16,20,23,24,27,32
 Seq#:105; Xaa Pos. 10,16,20,21,23,24
 Seq#:108; Xaa Pos. 16,20,21,23,24
 Seq#:111; Xaa Pos. 7,10,14,18,20,21,22,24,25
 Seq#:114; Xaa Pos. 6,14,18,21
 Seq#:117; Xaa Pos. 1,7,14,16,17,24,29,31,32,33,34
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 Seq#:123; Xaa Pos. 2,14,18,19,21,25,27,29
 Seq#:126; Xaa Pos. 2,15,19,20,22,23

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/058,053A

DATE: 07/23/2002
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Seq#:141; Xaa Pos. 10,16,20,21,23,24
Seq#:142; N Pos. 582
Seq#:144; Xaa Pos. 3,17,21,24,25,33,37
Seq#:147; Xaa Pos. 1,9,12,18
Seq#:150; Xaa Pos. 11,13,20,24,25,27,28
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Seq#:168; Xaa Pos. 3,13,14,17,21,23,24,25,33,37
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Seq#:174; Xaa Pos. 3,13,14,17,21,23,24,25,33,37
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Seq#:195; Xaa Pos. 9
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Seq#:201; Xaa Pos. 14,18,19,21,22
Seq#:204; Xaa Pos. 14,18,19,21,22
Seq#:207; Xaa Pos. 14,18,19,21,22,25
Seq#:210; Xaa Pos. 14,18,19,21,22,25,27,35,36
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Seq#:216; Xaa Pos. 2,15,19,20,22,23
Seq#:219; Xaa Pos. 2,15,19,20,22,23
Seq#:222; Xaa Pos. 7,11,16,17
Seq#:225; Xaa Pos. 11,13,20,24,25,27,28
Seq#:228; Xaa Pos. 7
Seq#:308; Xaa Pos. 4

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/058,053A

DATE: 07/23/2002
TIME: 15:59:20

Input Set : A:\2314-248-rev.ST25.txt
Output Set: N:\CRF3\07232002\J058053A.raw

Seq#:309; Xaa Pos. 5
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Seq#:313; Xaa Pos. 2
Seq#:314; Xaa Pos. 5
Seq#:315; Xaa Pos. 2,5
Seq#:316; Xaa Pos. 2
Seq#:317; Xaa Pos. 5
Seq#:318; Xaa Pos. 2,5
Seq#:319; Xaa Pos. 4
Seq#:320; Xaa Pos. 5
Seq#:321; Xaa Pos. 4
Seq#:323; Xaa Pos. 10
Seq#:324; Xaa Pos. 5
Seq#:325; Xaa Pos. 7
Seq#:326; Xaa Pos. 7
Seq#:327; Xaa Pos. 7
Seq#:328; Xaa Pos. 13
Seq#:329; Xaa Pos. 7
Seq#:330; Xaa Pos. 17
Seq#:331; Xaa Pos. 6
Seq#:332; Xaa Pos. 6
Seq#:333; Xaa Pos. 6
Seq#:336; Xaa Pos. 8
Seq#:337; Xaa Pos. 8
Seq#:338; Xaa Pos. 2,3,5
Seq#:339; Xaa Pos. 3